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        10            20            30            40            50            60            70            80            90
  GACGGATCGG    GAGATCTGCT    AGGTGACCTG    AGGCGCGCCG    GCTTCGAATA    GCCAGAGTAA    CCTTTTTTTT    TAATTTTATT    TTATTTTATT
  CTGCCTAGCC    CTCTAGACGA    TCCACTGGAC    TCCGCGCGGC    CGAAGCTTAT    CGGTCTCATT    GGAAAAAAAA    ATTAAAATAA    AATAAAATAA

       100           110           120           130           140           150           160           170           180
  TTTGAGATGG    AGTTTGGCGC    CGATCTCCCG    ATCCCCTATG    GTCGACTCTC    AGTACAATCT    GCTCTGATGC    CGCATAGTTA    AGCCAGTATC
  AAACTCTACC    TCAAACCGCG    GCTAGAGGGC    TAGGGGATAC    CAGCTGAGAG    TCATGTTAGA    CGAGACTACG    GCGTATCAAT    TCGGTCATAG

       190           200           210           220           230           240           250           260           270
  TGCTCCCTGC    TTGTGTGTTG    GAGGTCGCTG    AGTAGTGCGC    GAGCAAAATT    TAAGCTACAA    CAAGGCAAGG    CTTGACCGAC    AATTGCATGA
  ACGAGGGACG    AACACACAAC    CTCCAGCGAC    TCATCACGCG    CTCGTTTTAA    ATTCGATGTT    GTTCCGTTCC    GAACTGGCTG    TTAACGTACT

       280           290           300           310           320           330           340           350           360
  AGAATCTGCT    TAGGGTTAGG    CGTTTTGCGC    TGCTTCGCGA    TGTACGGGCC    AGATATACGC    GTTGACATTG    ATTATTGACT    AGTTATTAAT
  TCTTAGACGA    ATCCCAATCC    GCAAAACGCG    ACGAAGCGCT    ACATGCCCGG    TCTATATGCG    CAACTGTAAC    TAATAACTGA    TCAATAATTA

       370           380           390           400           410           420           430           440           450
  AGTAATCAAT    TACGGGGTCA    TTAGTTCATA    GCCCATATAT    GGAGTTCCGC    GTTACATAAC    TTACGGTAAA    TGGCCCGCCT    GGCTGACCGC
  TCATTAGTTA    ATGCCCCAGT    AATCAAGTAT    CGGGTATATA    CCTCAAGGCG    CAATGTATTG    AATGCCATTT    ACCGGGCGGA    CCGACTGGCG

       460           470           480           490           500           510           520           530           540
  CCAACGACCC    CCGCCCATTG    ACGTCAATAA    TGACGTATGT    TCCCATAGTA    ACGCCAATAG    GGACTTTCCA    TTGACGTCAA    TGGGTGGAGT
  GGTTGCTGGG    GGCGGGTAAC    TGCAGTTATT    ACTGCATACA    AGGGTATCAT    TGCGGTTATC    CCTGAAAGGT    AACTGCAGTT    ACCCACCTCA

       550           560           570           580           590           600           610           620           630
  ATTTACGGTA    AACTGCCCAC    TTGGCAGTAC    ATCAAGTGTA    TCATATGCCA    AGTACGCCCC    CTATTGACGT    CAATGACGGT    AAATGGCCCG
  TAAATGCCAT    TTGACGGGTG    AACCGTCATG    TAGTTCACAT    AGTATACGGT    TCATGCGGGG    GATAACTGCA    GTTACTGCCA    TTTACCGGGC

       640           650           660           670           680           690           700           710           720
  CCTGGCATTA    TGCCCAGTAC    ATGACCTTAT    GGGACTTTCC    TACTTGGCAG    TACATCTACG    TATTAGTCAT    CGCTATTACC    ATGGTGATGC
  GGACCGTAAT    ACGGGTCATG    TACTGGAATA    CCCTGAAAGG    ATGAACCGTC    ATGTAGATGC    ATAATCAGTA    GCGATAATGG    TACCACTACG

       730           740           750           760           770           780           790           800           810
  GGTTTTGGCA    GTACATCAAT    GGGCGTGGAT    AGCGGTTTGA    CTCACGGGGA    TTTCCAAGTC    TCCACCCCAT    TGACGTCAAT    GGGAGTTTGT
  CCAAAACCGT    CATGTAGTTA    CCCGCACCTA    TCGCCAAACT    GAGTGCCCCT    AAAGGTTCAG    AGGTGGGGTA    ACTGCAGTTA    CCCTCAAACA

       820           830           840           850           860           870           880           890           900
  TTTGGCACCA    AAATCAACGG    GACTTTCCAA    AATGTCGTAA    CAACTCCGCC    CCATTGACGC    AAATGGGCGG    TAGGCGTGTA    CGGTGGGAGG
  AAACCGTGGT    TTTAGTTGCC    CTGAAAGGTT    TTACAGCATT    GTTGAGGCGG    GGTAACTGCG    TTTACCCGCC    ATCCGCACAT    GCCACCCTCC
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FIGURE 14A
(SEQ ID NO. 10)

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910          920          930          940          950
TCTATATAAG   CAGAGCTCTC   TGGCTAACTA   GAGAACCCAC   TGCTTACTGG
AGATATATTC   GTCTCGAGAG   ACCGATTGAT   CTCTTGGGTG   ACGAATGACC

960          970          980          990
CTTATCGAAA   TTAATACGAC   TCACTATAGG   GAGACCCAAG
GAATAGCTTT   AATTATGCTG   AGTGATATCC   CTCTGGGTTC

1000         1010         1020         1030         1040
CTTGGTACCA   ATTTAAATTG   ATATCTCCTT   AGGTCTCGAG   TCTCTAGATA
GAACCATGGT   TAAATTTAAC   TATAGAGGAA   TCCAGAGCTC   AGAGATCTAT

1050         1060         1070         1080
ACCGGTCAAT   CGATTGGAAT   TCTTGCGGCC   GCTTGCTAGC
TGGCCAGTTA   GCTAACCTTA   AGAACGCCGG   CGAACGATCG

1090         1100         1110         1120         1130
CACCATGGAG   TTGTGGTTAA   GCTTGGTCCT   TCCTTGTCCT   TGTTTTAAAA
GTGGTACCTC   AACACCAATT   CGAACCAGGA   AGGAACAGGA   ACAAAATTTT

1140         1150         1160         1170
GGTGTCCAGT   GTGAAGTGAA   TCTGGTGGAG   TCTGGGGGAG
CCACAGGTCA   CACTTCACTT   AGACCACCTC   AGACCCCCTC

1180         1190         1200         1210         1220
GCTTAGTGCA   TCCCTGAGGG   TCCCTGAAAG   TCTCCTGTGT   AACCTCTGGA
CGAATCACGT   AGGGACTCCC   AGGGACTTTC   AGAGGACACA   TTGGAGACCT

1230         1240         1250         1260
TTCACTTTCA   GTGACTATTA   CATGTATTGG   GTTCGCCAGA
AAGTGAAAGT   CACTGATAAT   GTACATAACC   CAAGCGGTCT

1270         1280         1290         1300         1310
CTCCAGAGAA   GAGGCTGGAG   TGGGTCGCAT   ACATTAGTCA   AGGTGGTGAT
GAGGTCTCTT   CTCCGACCTC   ACCCAGCGTA   TGTAATCAGT   TCCACCACTA

1320         1330         1340         1350
ATAACCGACT   ATCCAGACAC   TGTAAAGGGT   CGATTCACCA
TATTGGCTGA   TAGGTCTGTG   ACATTTCCCA   GCTAAGTGGT

1360         1370         1380         1390         1400
TCTCCAGAGA   CAATGCCAAG   AACACCCTGT   ACCTGCAAAT   GAGCCGTCTG
AGAGGTCTCT   GTTACGGTTC   TTGTGGGACA   TGGACGTTTA   CTCGGCAGAC

1410         1420         1430         1440
AAGTCTGAGG   ACACAGCCAT   GTATTACTGT   GCAAGAGGCC
TTCAGACTCC   TGTGTCGGTA   CATAATGACA   CGTTCTCCGG

1450         1460         1470         1480         1490
TGGACGACGG   GGCCTGGTTT   GCTTACTGGG   GCCAAGGGAC   TCTGGTCACG
ACCTGCTGCC   CCGGACCAAA   CGAATGACCC   CGGTTCCCTG   AGACCAGTGC

1500         1510         1520         1530
CTAGCACCAA   GGGCCCATCG   GTCTTCCCCC   GTGGTCACCG
GATCGTGGTT   CCCGGGTAGC   CAGAAGGGGG   CACCAGTGGC

1540         1550         1560         1570         1580
TGGCACCCTC   CTCCAAGAGC   ACCTCTGGGG   GCACAGCGGC   CCTGGGCTGC
ACCGTGGGAG   GAGGTTCTCG   TGGAGACCCC   CGTGTCGCCG   GGACCCGACG

1590         1600         1610         1620
CTGGTCAAGG   ACTACTTCCC   CGAACCGGTG   ACGGTGTCGT
GACCAGTTCC   TGATGAAGGG   GCTTGGCCAC   TGCCACAGCA

1630         1640         1650         1660         1670
GGAACTCAGG   CGCCCTGACC   AGCGGCGTGC   ACACCTTCCC   GGCTGTCCTA
CCTTGAGTCC   GCGGGACTGG   TCGCCGCACG   TGTGGAAGGG   CCGACAGGAT

1680         1690         1700         1710
CAGTCCTCAG   GACTCTACTC   CCTCAGCAGC   GTGGTGACCG
GTCAGGAGTC   CTGAGATGAG   GGAGTCGTCG   CACCACTGGC

1720         1730         1740         1750         1760
TGCCCTCCAG   CAGCTTGGGC   ACCCAGACCT   ACATCTGCAA   CGTGAATCAC
ACGGGAGGTC   GTCGAACCCG   TGGGTCTGGA   TGTAGACGTT   GCACTTAGTG

1770         1780         1790         1800
AAGCCCAGCA   ACACCAAGGT   GGACAAGAAA   GTTGGTGAGA
TTCGGGTCGT   TGTGGTTCCA   CCTGTTCTTT   CAACCACTCT
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FIGURE 14B
(SEQ ID NO. 10)

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      1810       1820       1830       1840       1850       1860       1870       1880       1890
GGCCAGCACA GGGAGGGAGG GTGTCTGCTG GAAGCCAGGC TCAGGCGCTC TGCCTGGACG CATCCCGGCT ATGCAGCCCC AGTCCAGGGC
CCGGTCGTGT CCCTCCCTCC CACAGACGAC CTTCGGTCCG AGTCCGCGAG ACGGACCTGC GTAGGGCCGA TACGTCGGGG TCAGGTCCCG

      1900       1910       1920       1930       1940       1950       1960       1970       1980
AGCAAGGCAG GCCCCGTCTG CCTCTTCACC CGGAGGCCTC TGCCCGCCCC ACTCATGCTC AGGGAGAGGG TCTTCTGGCT TTTTCCCCAG
TCGTTCCGTC CGGGGCAGAC GGAGAAGTGG GCCTCCGGAG ACGGGCGGGG TGAGTACGAG TCCCTCTCCC AGAAGACCGA AAAAGGGGTC

      1990       2000       2010       2020       2030       2040       2050       2060       2070
GCTCTGGGCA GGCACAGGCT AGGTGCCCCT AACCCAGGCC CTGCACACAA AGGGGCAGGT GCTGGGCTCA GACCTGCCAA GAGCCATATC
CGAGACCCGT CCGTGTCCGA TCCACGGGGA TTGGGTCCGG GACGTGTGTT TCCCCGTCCA CGACCCGAGT CTGGACGGTT CTCGGTATAG

      2080       2090       2100       2110       2120       2130       2140       2150       2160
CGGGAGGACC CTGCCCCTGA CCTAAGCCCA CCCCAAAGGC CAAACTCTCC ACTCCCTCAG CTCGGACACC TTCTCTCCTC CCAGATTCCA
GCCCTCCTGG GACGGGGACT GGATTCGGGT GGGGTTTCCG GTTTGAGAGG TGAGGGAGTC GAGCCTGTGG AAGAGAGGAG GGTCTAAGGT

      2170       2180       2190       2200       2210       2220       2230       2240       2250
GTAACTCCCA ATCTTCTCTC TGCAGAGCCC AAATCTTGTG ACAAAACTCA CACATGCCCA CCGTGCCCAG GTAAGCCAGC CCAGGCCTCG
CATTGAGGGT TAGAAGAGAG ACGTCTCGGG TTTAGAACAC TGTTTTGAGT GTGTACGGGT GGCACGGGTC CATTCGGTCG GGTCCGGAGC

      2260       2270       2280       2290       2300       2310       2320       2330       2340
CCCTCCAGCT CAAGGCGGGA CAGGTGCCCT AGAGTAGCCT GCATCCAGGG ACACACCACG TGGGTACCAA CATGTCCGGA GCCACATGGA
GGGAGGTCGA GTTCCGCCCT GTCCACGGGA TCTCATCGGA CGTAGGTCCC TGTGTGGTGC ACCCATGGTT GTACAGGCCT CGGTGTACCT

      2350       2360       2370       2380       2390       2400       2410       2420       2430
CAGAGGCCGG CTCGGCCCAC CCTCTGCCCT GAGAGTGACC GCTGTACCAA CCTCTGTCCC TACAGGGCAG CCCGAGAAAC CACAGGTGTA
GTCTCCGGCC GAGCCGGGTG GGAGACGGGA CTCTCACTGG CGACATGGTT GGAGACAGGG ATGTCCCGTC GGGCTCTTTG GTGTCCACAT

      2440       2450       2460       2470       2480       2490       2500       2510       2520
CACCCTGCCC CCATCCCGGG ATGAGCTGAC CAAGAACCAG GTCAGCCTGA CCTGCCTGGT CAAAGGCTTC TATCCCAGCG ACATCGCCGT
GTGGGACGGG GGTAGGGCCC TACTCGACTG GTTCTTGGTC CAGTCGGACT GGACGGACCA GTTTCCGAAG ATAGGGTCGC TGTAGCGGCA

      2530       2540       2550       2560       2570       2580       2590       2600       2610
GGAGTGGGAG AGCAATGGGC AGCCGGAGAA CAACTACAAG ACCACGCCTC CTCCGACGGC CCGTGCTGGA TCCTTCTTCC TCTACAGCAA
CCTCACCCTC TCGTTACCCG TCGGCCTCTT GTTGATGTTC TGGTGCGGAG GAGGCTGCCG GGCACGACCT AGGAAGAAGG AGATGTCGTT

      2620       2630       2640       2650       2660       2670       2680       2690       2700
GCTCACCGTG GACAAGAGCA GGTGGCAGCA TTCTCATGCT CCGTGATGCA TGAGGCTCTG CACAACCACT ACACGCAGAA
CGAGTGGCAC CTGTTCTCGT CCACCGTCGT AAGAGTACGA GGCACTACGT ACTCCGAGAC GTGTTGGTGA TGTGCGTCTT
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FIGURE 14C
(SEQ ID NO. 10)

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2710       2720       2730       2740       2750       2760       2770       2780       2790
GAGCCTCTCC CTGTCTCCGG GTAAATGAGT GCGACGGCCG GCAAGCCCCC GCTCCCCGGG CTCTTCGCGGT CGCACGAGGA TGCTTGGCAC
CTCGGAGAGG GACAGAGGCC CATTTACTCA CGCTGCCGGC CGTTCGGGGG CGAGGGGCCC GAGAGCGCCA GCGGTGCTCCT ACGAACCGTG

2800       2810       2820       2830       2840       2850       2860       2870       2880
GTACCCCCTG TACATACTTC CCGGGGCGCCC AGCATGGAAA TAAAGCACCC AGCGGCTGCCC TGGGCCCCTG CGAGACTGTG ATGGTTCTTT
CATGGGGGAC ATGTATGAAG GGCCCCGCGGG TCGTACCTTT ATTTCGTGGG TCGCCGACGGG ACCCGGGGAC GCTCTGACAC TACCAAGAAA

2890       2900       2910       2920       2930       2940       2950       2960       2970
CCACGGGTCA GGCCGAGTCT GAGGCCTGAG TGGCATGAGG GAGGCAGAGC GGGTCCCACT GTCCCCACAC TGGCCCAGGC TGTGCAGGTG
GGTGCCCAGT CCGGCTCAGA CTCCGGACTC ACCGTACTCC CTCCGTCTCG CCCAGGGTGA CAGGGGTGTG ACCGGGTCCG ACACGTCCAC

2980       2990       3000       3010       3020       3030       3040       3050       3060
TGCCTGGGCC CCCTAGGGTG GGGCTCAGCC AGGGGCTGCC CTCGGCAGGG TGGGGGATTT GCCAGCGTGG CCCTCCCTCC AGCAGCACCT
ACGGACCCGG GGGATCCCAC CCCGAGTCGG TCCCCGACGG GAGCCGTCCC ACCCCCTAAA CGGTCGCACC GGGAGGGAGG TCGTCGTGGA

3070       3080       3090       3100       3110       3120       3130       3140       3150
GCCCTGGGCT GGGCCACGGG AAGCCCCTAGG AGCCCCCTGGG GACAGACACA CAGCCCCTGC CTCTGTAGGA GACTGTCCTG TTCTGTGAGC
CGGGACCCGA CCCGGTGCCC TTCGGGGATCC TCGGGGGACCC CTGTCTGTGT GTCGGGGACG GAGACATCCT CTGACAGGAC AAGACACTCG

3160       3170       3180       3190       3200       3210       3220       3230       3240
GCCCCTGTCC TCCCGACCTC CATGCCCACT CGGGGGCATG CCTAGTCCAT GTGCGTAGGG ACAGGCCCTC CCTCACCCAT CTACCCCCAC
CGGGGACAGG AGGGCTGGAG GTACGGGTGA GCCCCCGTAC GGATCAGGTA CACGCATCCC TGTCCGGGAG GGAGTGGGTG GATGGGGGTG

3250       3260       3270       3280       3290       3300       3310       3320       3330
GGCACTAACC CCTGGCTGCC CTGCCCAGCC TCGCACCCGC ATGGGGACAC AACCGACTCC GGGGACATGC ACTCTCGGGC CCTCGTGAGG
CCGTGATTGG GGACCGACGG GACGGGTCGG AGCGTGGGCG TACCCCTGTG TTGGCTGAGG CCCCTGTACG TGAGAGCCCG GGACACTCC

3340       3350       3360       3370       3380       3390       3400       3410       3420
GACTGGTGCA GATGCCCACA CACACACTCA GCCCAGACCC GTTCAACAAA CCCCGCACTG AGGTTGGCCG GCCACACGGC CACCACACAC
CTGACCACGT CTACGGGTGT GTGTGTGAGT CGGGTCTGGG CAAGTTGTTT GGGGCGTGAC TCCAACCGGC CGGTGTGCCG GTGGTGTGTG

3430       3440       3450       3460       3470       3480       3490       3500       3510
ACACGTGCAC GCCTCACACA CGGAGCCTCA CCCGGGGCGAA CTGCACAGCA CCCAGACCAG AGCAAGGTCC TCGCACACGT GAACACTCCT
TGTGCACGTG CGGAGTGTGT GCCTCGGAGT GGGCCCCGCTT GACGTGTCGT GGGTCTGGTC TCGTTCCAGG AGCGTGTGCA CTTGTGAGGA

3520       3530       3540       3550       3560       3570       3580       3590       3600
CGGACACAGG CCCCCACGCGG CACCTCAAGG CCCACGAGCC TTCTCGGCAGC TTCTCCACAT GCTGACCTGC TCAGACAAAC
GCCTGTGTCC GGGGGTGCGCC GTGGAGTTCC GGGTGCTCGG AAGAGCCGTCG AAGAGGTGTA CGACTGGACG AGTCTGTTTG
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FIGURE 14D
(SEQ ID NO. 10)

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       3610       3620       3630       3640       3650       3660       3670       3680       3690
 CCAGCCCTCC TCTCACAAGG GTGCCCCTGC AGCCGCCACA CACACACAGG GGATCACACA CCACGTCACG TCCCTGGCCC TGGCCCACTT
 GGTCGGGAGG AGAGTGTTCC CACGGGGACG TCGGCGGTGT GTGTGTGTCC CCTAGTGTGT GGTGCAGTGC AGGGACCGGG ACCGGGTGAA

       3700       3710       3720       3730       3740       3750       3760       3770       3780
 CCCAGTGCCG CCCTTCCCTG CAGGACGGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT
 GGGTCACGGC GGGAAGGGAC GTCCTGCCTA GTCGGAGCTG ACACGGAAGA TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA

       3790       3800       3810       3820       3830       3840       3850       3860       3870
 CCTTGACCCT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAATGAG GAAATTGCAT CGCATTGTCT GAGTAGGTGT CATTCTATTC
 GGAACTGGGA CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC CTTTAACGTA GCGTAACAGA CTCATCCACA GTAAGATAAG

       3880       3890       3900       3910       3920       3930       3940       3950       3960
 TGGGGGTGG  GGTGGGGCAG GACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG CTGGGGATGC GGTGGGCTCT ATGGCTTCTG
 ACCCCCCACC CCACCCCGTC CTGTCGTTCC CCCTTCTAAC CCTTCTGTTA TCGTCCGTAC GACCCCTACG CCACCCGAGA TACCGAAGAC

       3970       3980       3990       4000       4010       4020       4030       4040       4050
 AGGGCGAAAG AACCAGCTGG GGCTCTAGGG GGTATCCCCA CGCGCCCTGT AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGGCGA
 TCCGCCTTTC TTGGTCGACC CCGAGATCCC CCATAGGGGT GCGCGGGACA TCGCCGCCGTA ATTCGCGCCG CCCACCACAC CAATGCGCGT

       4060       4070       4080       4090       4100       4110       4120       4130       4140
 GCGTGACCGC TACACTTGCC AGCGCCCTAG CGCCCGCTCC TTTCGCTTTC TTCCCTTCCT TTCTCGCCAC GTTCGCCGGG CCTCTCAAA
 CGCACTGGCG ATGTGAACGG TCGCGGGATC GCGGGCGAGG AAAGCGAAAG AAGGGAAGGA AAGAGCGGTG CAAGCGCGCC GGAGAGTTTT

       4150       4160       4170       4180       4190       4200       4210       4220       4230
 AAGGGAAAAA AAGCATGCAT CTCAATTAGT CAGCAACCAT AGTCCCGCCC CCATCCCGCC CCAATCCGCC CCTAACTCCG CCCAGTTCCG
 TTCCCTTTTT TTCGTACGTA GAGTTAATCA GTCGTTGGTA TCAGGGCGGG GGTAGGGCGG GGTTAGGCGG GGATTGAGGC GGGTCAAGGC

       4240       4250       4260       4270       4280       4290       4300       4310       4320
 CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTTATTTA TGCAGAGGCC GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG
 GGGTAAGAGG CGGGGTACCG ACTGATTAAA AAAATAAAT  ACGTCTCCGG CTCCGGCGGA GCCGGAGACT CGATAAGGTC TTCATCACTC

       4330       4340       4350       4360       4370       4380       4390       4400       4410
 GAGGCTTTTT TGGAGGCCTA GGCTTTTGCA AAAAGCTTGG ACAGCTCAGG GCTGCGATTT CGCGCCAAAC TTGACGGCAA TCCTAGCGTG
 CTCCGAAAAA ACCTCCGGAT CCGAAAAACGT TTTTCGAACC TGTCGAGTCC CGACGCTAAA GCGCGGTTTG AACTGCCGTT AGGATCGCAC

       4420       4430       4440       4450       4460       4470       4480       4490       4500
 AAGGCTGGTA GGATTTTATC CCCGCTGCCA TCATGGTTCG ACCATTGAAC TGCATCGTCG CCGTGTCCCA AAATATGGGG ATTGGCAAGA
 TTCCGACCAT CCTAAAATAG GGGCGACGGT AGTACCAAGC TGGTAACTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT
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FIGURE 14E
(SEQ ID NO. 10)

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    4510       4520       4530       4540       4550       4560       4570       4580       4590
ACGGAGACCT ACCCTGGCCT CCGCTCAGGA ACGAGTTCAA GTACTTCCAA AGAATGACCA CAACCTCTTC AGTGGAAGGT AAACAGAATC
TGCCTCTGGA TGGGACCGGA GGCGAGTCCT TGCTCAAGTT CATGAAGGTT TCTTACTGGT GTTGGAGAAG TCACCTTCCA TTTGTCTTAG

    4600       4610       4620       4630       4640       4650       4660       4670       4680
TGGTGATTAT GGGTAGGAAA ACCTGGTTCT CCATTCCTGA GAAGAATCGA CCTTTAAAGG ACAGAATTAA TATAGTTCTC AGTAGAGAAC
ACCACTAATA CCCATCCTTT TGGACCAAGA GGTAAGGACT CTTCTTAGCT GGAAAATTCC TGTCTTAATT ATATCAAGAG TCATCTCTTG

    4690       4700       4710       4720       4730       4740       4750       4760       4770
TCAAAGAACC ACCACGAGGA GCTCATTTTC TTGCCAAAAG TTTGGATGAT GCCTTAAGAC TTATTGAACA ACCGGAATTG GCAAGTAAAG
AGTTTCTTGG TGGTGCTCCT CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG AATAACTTGT TGGCCTTAAC CGTTCATTTC

    4780       4790       4800       4810       4820       4830       4840       4850       4860
TAGACATGGT TTGGATAGTC GGAGGCAGTT CTGTTTACCA GGAAGCCATG AATCAACCAG GCCACCTTAG ACTCTTTGTG ACAAGGATCA
ATCTGTACCA AACCTATCAG CCTCCGTCAA GACAAATGGT CCTTCGGTAC TTAGTTGGTC CGGTGGAATC TGAGAAACAC TGTTCCTAGT

    4870       4880       4890       4900       4910       4920       4930       4940       4950
TGCAGGAATT TGAAAGTGAC ACGTTTTTCC CAGAAAATGA TTTGGGGAAA TATAAACTTC TCCCAGAATA CCCAGGCGTC CTCTCTGAGG
ACGTCCTTAA ACTTTCACTG TGCAAAAAGG GTCTTTAACT AAACCCCTTT ATATTTGAAG AGGGTCTTAT GGGTCCGCAG GAGAGACTCC

    4960       4970       4980       4990       5000       5010       5020       5030       5040
TCCAGGAGGA AAAAGGCATC AAGTATAAGT TTGAAGTCTA CGAGAAGAAA GACTAACAGG AAGATGCTTT CAAGTTCTCT GCTCCCCTCC
AGGTCCTCCT TTTTCCGTAG TTCATATTCA AACTTCAGAT GCTCTTCTTT CTGATTGTCC TTCTACGAAA GTTCAAGAGA CGAGGGGAGG

    5050       5060       5070       5080       5090       5100       5110       5120       5130
TAAAGCTATG CATTTTTATA AGACCATGGG ACTTTTGCTG GCTTTAGATC TCTTTGTGAA GGAACCTTAC TTCTGTGGTG TGACATAATT
ATTTCGATAC GTAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT CCTTGGAATG AAGACCACCAC ACTGTATTAA

    5140       5150       5160       5170       5180       5190       5200       5210       5220
GGACAAACTA CCTACAGAGA TTTAAAGCTC TAAGGTAAAT ATAAAATTTT TAAGTGTATA ATGTGTTAAA CTACTGATTC TAATTGTTTG
CCTGTTTGAT GGATGTCTCT AAATTTCGAG ATTCCATTTA TATTTTAAAA ATTCACATAT TACACAATTT GATGACTAAG ATTAACAAAC

    5230       5240       5250.      5260       5270       5280       5290       5300       5310
TGTATTTTAG ATTCCAACCT ATGGAACTGA TGAATGGGAG CAGTGGTGGA ATGCCTTTAA TGAGGAAAAC CTGTTTTGCT CAGAAGAAAT
ACATAAAAATC TAAGGTTGGA TACCTTGACT ACTTACCCTC GTCACCACCT TACGGAAATT ACTCCTTTTG GACAAAACGA GTCTTCTTTA

    5320       5330       5340       5350       5360       5370       5380       5390       5400
GCCATCTAGT GATGATGAGG CTACTGCTGA CTCTCAACAT TCTACTCCTC CAAAAAAGAA GAGAAAGGTA GAAGACCCCA AGGACTTTCC
CGGTAGATCA CTACTACTCC GATGACGACT GAGAGTTGTA AGATGAGGAG GTTTTTTCTT CTCTTTCCAT CTTCTGGGGT TCCTGAAAGG
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FIGURE 14F
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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5410        5420        5430        5440        5450        5460        5470        5480        5490
TTCAGAATTG  CTAAGTTTTT  TGAGTCATGC  TGTGTTTAGT  AATAGAACTC  TTGCTTGCTT  TGCTATTTAC  ACCACAAAGG  AAAAAGCTGC
AAGTCTTAAC  GATTCAAAAA  ACTCAGTACG  ACACAAATCA  TTATCTTGAG  AACGAACGAA  ACGATAAATG  TGGTGTTTCC  TTTTTCGACG

5500        5510        5520        5530        5540        5550        5560        5570        5580
ACTGCTATAC  AAGAAAATTA  TGGAAAAATA  TTCTGTAACC  TTTATAAGTA  GGCATAACAG  TTATAATCAT  AACATACTGT  TTTTTCTTAC
TGACGATATG  TTCTTTTTAT  ACCTTTTTAT  AAGACATTGG  AAATATTCAT  CCGTATTGTC  AATATTAGTA  TTGTATGACA  AAAAAGAATG

5590        5600        5610        5620        5630        5640        5650        5660        5670
TCCACACAGG  CATAGAGTGT  CTGCTATTAA  TAACTATGCT  CAAAAATTGT  GTACCTTTAG  TGTAAAGGGG  TTAATAAGGA
AGGTGTGTCC  GTATCTCACA  GACGATAATT  ATTGATACGA  GTTTTTAACA  CATGGAAATC  ACATTTCCCC  AATTATTCCT

5680        5690        5700        5710        5720        5730        5740        5750        5760
ATATTTGATG  TATAGTGCCT  TGACTAGAGA  TCATAATCAG  CCATACCACA  TTTGTAGAGG  TTTTACTTGC  TTTAAAAAAC  CTCCCACACC
TATAAACTAC  ATATCACGGA  ACTGATCTCT  AGTATTAGTC  GGTATGGTGT  AAACATCTCC  AAAATGAACG  AAATTTTTTG  GAGGGTGTGG

5770        5780        5790        5800        5810        5820        5830        5840        5850
TCCCCCTGAA  CCTGAAACAT  AAAATGAATG  CAATTGTTGT  TGTTAACTTG  TTTATTGCAG  CTTATAATGG  TTACAAATAA  AGCAATAGCA
AGGGGGACTT  GGACTTTGTA  TTTTACTTAC  GTTAACAACA  ACAATTGAAC  AAATAACGTC  GAATATTACC  AATGTTTATT  TCGTTATCGT

5860        5870        5880        5890        5900        5910        5920        5930        5940
TCACAAATTT  CACAAATAAA  GCATTTTTTT  CACTGCATTC  TAGTTGTGGT  TTGTCCAAAC  TCATCAATGT  ATCTTATCAT  GTCTCGATCG
AGTGTTTAAA  GTGTTTATTT  CGTAAAAAAA  GTGACGTAAG  ATCAACACCA  AACAGGTTTG  AGTAGTTACA  TAGAATAGTA  CAGACCTAGC

5950        5960        5970        5980        5990        6000        6010        6020        6030
GCTGGATGAT  CCTCCAGCGC  GGGGATCTCA  TGCTGGAGTT  CTTCGCCCAC  CCCAACTTGT  TTATTGCAGC  TTATAATGGT  TACAAATAAA
CGACCTACTA  GGAGGTCGCG  CCCCTAGAGT  ACGACCTCAA  GAAGCGGGTG  GGGTTGAACA  AATAACGTCG  AATATTACCA  ATGTTTATTT

6040        6050        6060        6070        6080        6090        6100        6110        6120
GCAATAGCAT  CACAAATTTC  ACAAATAAAG  CATTTTTTTC  ACTGCATTCT  AGTTGTGGTT  TGTCCAAACT  CATCAATGTA  TCTTATCATG
CGTTATCGTA  GTGTTTAAAG  TGTTTATTTC  GTAAAAAAAG  TGACGTAAGA  TCAACACCAA  ACAGGTTTGA  GTAGTTACAT  AGAATAGTAC

6130        6140        6150        6160        6170        6180        6190        6200        6210
TCTGTATACC  GTCGACCTCT  AGCTAGAGCT  TGGCGTAATC  ATGGTCATAG  CTGTTTCCTG  TGTGAAATTG  TTATCCGCTC  ACAATTCCAC
AGACATATGG  CAGCTGGAGA  TCGATCTCGA  ACCGCATTAG  TACCAGTATC  GACAAAGGAC  AATAGGCGAG  ACACTTTAAC  TGTTAAGGTG

6220        6230        6240        6250        6260        6270        6280        6290        6300
ACAACATACG  AGCCGGAAGC  ATAAAGTGTA  AAGCCTGGGG  TGCCTAATGA  GTGAGCTAAC  TCACATTAAT  TGCGTTGCGC  TCACTGCCCG
TGTTGTATGC  TCGGCCTTCG  TATTTCACAT  TTCGGACCCC  ACGGATTACT  CACTCGATTG  AGTGTAATTA  ACGCAACGCG  AGTGACGGGC
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FIGURE 14G
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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      6310       6320       6330       6340       6350       6360       6370       6380       6390
CTTTCCAGTC GGGAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGCGCGGGGA GAGGCGGTTT GCGTATTGGG CGCTCTTCCG
GAAAGGTCAG CCCTTTGGAC AGCACGGTCG ACGTAATTAC TTAGCCGGTT GCGCGCCCCT CTCCGCCAAA CGCATAACCC GCGAGAAGGC

      6400       6410       6420       6430       6440       6450       6460       6470       6480
CTTCCTCGCT CACTGACTCG CTGCGCTCGG TCGTTCGGCT GCGGGCGACG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
GAAGGAGCGA GTGACTGAGC GACGCGAGCC AGCAAGCCGA CGCCGCTGCC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC

      6490       6500       6510       6520       6530       6540       6550       6560       6570
AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC
TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC CGGTCCTTGG CATTTTTCCG GCGCAACGAC CGCAAAAAGG

      6580       6590       6600       6610       6620       6630       6640       6650       6660
ATAGGCTCCG CCCCCCTGAC GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT
TATCCGAGGC GGGGGACTG CTCGTAGTGT TTTTAGCTGC GAGTTCGTGC TCCACCGCTT TGGGCTGTCC TGATATTTCT ATGGTCCGCA

      6670       6680       6690       6700       6710       6720       6730       6740       6750
TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG
AAGGGGGACC TTCGAGGGAG CACGCGGGAG GACAAGGCTG GGACGGCCGA TGGCCTATGG ACAGGGCGGAA AGAGGGAAGC CCTTCGCACC

      6760       6770       6780       6790       6800       6810       6820       6830       6840
CGCTTTCTCA ATGCTCACGC TGTAGGTATC TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC
GCGAAAGAGT TACGAGTGCG ACATCCATAG AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG GGGCAAGTCG

      6850       6860       6870       6880       6890       6900       6910       6920       6930
CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA
GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG GTTGGGCCAT TCTGTGCTGA ATAGCGGTGA CCGTCGTCGG TGACCATTGT

      6940       6950       6960       6970       6980       6990       7000       7010       7020
GGATTAGCAG AGGGAGGTAT GTAGGCGGTG CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA
CCTAATCGTC TCGCTCCATA CATCCGCCAC GATGTCTCAA GAACTTCACC ACCGGATTGA TGCCGATGTG ATCTTCCTGT CATAAACCAT

      7030       7040       7050       7060       7070       7080       7090       7100       7110
TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA AACAAACCAC CGCTGGTAGC GGTGGTTTTT
AGACGCGAGA CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT TTGTTTGGTG GCGACCATCG CCACCAAAAA

      7120       7130       7140       7150       7160       7170       7180       7190       7200
TTGTTTGCAA GCAGCAGATT ACCGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAACG
AACAAACGTT CGTCGTCTAA TGGCGCGTCTT TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC CAGACTGCGA GTCACCTTGC
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FIGURE 14H
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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7210  AAAACTCACG   7220  TTAAGGGATT   7230  TTGGTCATGA   7240  GATTATCAAA   7250  AAGGATCTTC
      TTTTGAGTGC         AATTCCCTAA         AACCAGTACT         CTAATAGTTT         TTCCTAGAAG

7260  ACCTAGATCC   7270  TTTTAAATTA   7280  AAAATGAAGT   7290  TTTAAATCAA
      TGGATCTAGG         AAAATTTAAT         TTTTACTTCA         AAATTTAGTT

7300  TCTAAAGTAT   7310  ATATGAGTAA   7320  ACTTGGTCTG   7330  ACAGTTACCA   7340  ATGCTTAATC
      AGATTTCATA         TATACTCATT         TGAACCAGAC         TGTCAATGGT         TACGAATTAG

7350  AGTGAGGCAC   7360  CTATCTCAGC   7370  GATCTGTCTA   7380  TTTCGTTCAT
      TCACTCCGTG         GATAGAGTCG         CTAGACAGAT         AAAGCAAGTA

7390  CCATAGTTGC   7400  CTGACTCCCC   7410  GTCGTGTAGA   7420  TAACTACGAT   7430  ACGGGAGGGC
      GGTATCAACG         GACTGAGGGG         CAGCACATCT         ATTGATGCTA         TGCCCTCCCG

7440  TTACCATCTG   7450  GCCCCAGTGC   7460  TGCAATGATA   7470  CCGGAGACC
      AATGGTAGAC         CGGGGTCACG         ACGTTACTAT         GGCGCTCTGG

7480  CACGCTCACC   7490  GGCTCCAGAT   7500  TTATCAGCAA   7510  TAAACCAGCC   7520  AGCCGGAAGG
      GTGCGAGTGG         CCGAGGTCTA         AATAGTCGTT         ATTTGGTCGG         TCGGCCTTCC

7530  GCCGAGCGCA   7540  GAAGTGGTCC   7550  TGCAACTTTA   7560  TCCGCCTCCA
      CGGCTCGCGT         CTTCACCAGG         ACGTTGAAAT         AGGCGGAGGT

7570  TCCAGTCTAT   7580  TAATTGTTGC   7590  CGGGAAGCTA   7600  GAGTAAGTAG   7610  TTCGCCAGTT
      AGGTCAGATA         ATTAACAACG         GCCCTTCGAT         CTCATTCATC         AAGCGGTCAA

7620  AATAGTTTGC   7630  GCAACGTTGT   7640  TGCCATTGCT   7650  ACAGGCATCG
      TTATCAAACG         CGTTGCAACA         ACGGTAACGA         TGTCCGTAGC

7660  CTCGTCGTTG   7670  GGTATGGCTT   7680  CATTCAGCTC   7690  CGGTTCCCAA   7700  CGATCAAGGC
      GAGCAGCAAC         CCATACCGAA         GTAAGTCGAG         GCCAAGGGTT         GCTAGTTCCG

7710  GAGTTACATG   7720  ATCCCCCATG   7730  ATCCCCCATG   7740  GTTGTGCAAAA
      CTCAATGTAC         TAGGGGGTAC         TAGGGGGTAC         AACACGTTTT

7750  AAGCGGTTAG   7760  CTCCTTCGGT   7770  CCTCCGATCG   7780  TTGTCAGAAG   7790  TAAGTTGGCC
      TTCGCCAATC         GAGGAAGCCA         GGAGGCTAGC         AACAGTCTTC         ATTCAACCGG

7800  GCAGTGTTAT   7810  CACTCATGGT   7820  TATGGCAGCA   7830  CTGCATAATT
      CGTCACAATA         GTGAGTACCA         ATACCGTCGT         GACGTATTAA

7840  CTCTTACTGT   7850  CATGCCATCC   7860  GTAAGATGCT   7870  TTTCTGTGAC   7880  TGGTGAGTAC
      GAGAATGACA         GTACGGTAGG         CATTCTACGA         AAAGACACTG         ACCACTCATG

7890  TCAACCAAGT   7900  CATTCTGAGA   7910  ATAGTGTATG   7920  CGGGACCGA
      AGTTGGTTCA         GTAAGACTCT         TATCACATAC         GCCGCTGGCT

7930  GTTGCTCTTG   7940  CCCGGCGTCA   7950  ATACGGGATA   7960  ATACCGCGCC   7970  ACATAGCAGA
      CAACGAGAAC         GGGCCGCAGT         TATGCCCTAT         TATGGCGCGG         TGTATCGTCT

7980  ACTTTAAAAG   7990  TGCTCATCAT   8000  TGGAAAACGT   8010  TCTTCGGGGC
      TGAAATTTTC         ACGAGTAGTA         ACCTTTTGCA         AGAAGCCCCG

8020  GAAAACTCTC   8030  AAGGANCTTA   8040  CCGCTGTTGA   8050  GATCCAGTTC   8060  GATGTAACCC
      CTTTTGAGAG         TTCCTAGAAT         GGCGACAACT         CTAGGTCAAG         CTACATTGGG

8070  ACTCGTGCAC   8080  CCAACTGATC   8090  TTCAGCATCT   8100  TTTACTTTCA
      TGAGCACGTG         GGTTGACTAG         AAGTCGTAGA         AAATGAAAGT
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FIGURE 14I
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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           8110       8120       8130       8140       8150       8160       8170       8180       8190
     CCAGCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT
     GGTCGCAAAG ACCCACTCGT TTTTGTCCTT CCGTTTTACG GCGTTTTTTC CCTTATTCCC GCTGTGCCTT TACAACTTAT GAGTATGAGA

           8200       8210       8220       8230       8240       8250       8260       8270       8280
     TCCTTTTTCA ATATTATTGA AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
     AGGAAAAAGT TATAATAACT TCGTAAATAG TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC

           8290       8300       8310       8320       8330
     GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT C
     CCCAAGGCGC GTGTAAAGGG GCTTTTCACG GTGGACTGCA G
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FIGURE 14J
SEQ ID NO. 10)

FIGURE 18A (SEQ ID NO. 22)

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   1  GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC

  51  GGTCAATCGA TTGGAATTCT TGCGGCCGCT TGCTAGCCAC CATGGAGTTG

 101  TGGTTAAGCT TGGTCTTCCT TGTCCTTGTT TTAAAAGGTG TCCAGTGTGA

 151  AGTGCAACTG GTGGAGTCTG GGGGAGGCTT AGTGCAGCCT GGAGGGTCCC

 201  TGCGACTTTC CTGTGCTGCA TCTGGATTCC CGTTCAGTGA CTATTACATG

 251  TATTGGGTTC GCCAGGCTCC AGGCAAGGGA CTGGAGTGGG TCTCATACAT

 301  TAGTCAAGAT GGTGATATAA CCGACTATGC AGACTCCGTA AAGGGTCGAT

 351  TCACCATCTC CAGAGACAAT GCAAGAACA GCCTGTACCT GCAAATGAAC

 401  AGCCTGAGGG ACGAGGACAC AGCCGTGTAT TACTGTGCAA GAGGCCTGGC

 451  GGACGGGGCC TGGTTTGCTT ACTGGGGCCA AGGGACTCTG GTCACGGTCT

 501  CTTCCGCTAG CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC

 551  AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA

 601  CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG

 651  GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC

 701  AGCAGCGTGG TCACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT

 751  CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC AAGAAAGTTG

 801  GTGAGAGGCC AGCACAGGGA GGGAGGGTGT CTGCTGGAAG CCAGGCTCAG

 851  CGCTCCTGCC TGGACGCATC CCGGCTATGC AGCCCCAGTC CAGGGCAGCA

 901  AGGCAGGCCC CGTCTGCCTC TTCACCCGGA GGCCTCTGCC CGCCCCACTC

 951  ATGCTCAGGG AGAGGGTCTT CTGGCTTTTT CCCCAGGCTC TGGGCAGGCA

1001  CAGGCTAGGT GCCCCTAACC CAGGCCCTGC ACACAAAGGG GCAGGTGCTG

1051  GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC CCCTGACCTA

1101  AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT

1151  CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT

1201  CTTGTGACAA AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG

1251  GCCTCGCCCT CCAGCTCAAG GCGGGACAGG TGCCCTAGAG TAGCCTGCAT

1301  CCAGGGACAG GCCCCAGCCG GGTGCTGACA CGTCCACCTC CATCTCTTCC
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235      237
1351  TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT TCCCCCCAAA

1401  ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG

1451  TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG

1501  GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA

1551  CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT
                            318      320  322
1601  GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA
        331
1651  GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA CCCGTGGGGT

1701  GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA

1751  GTGACCGCTG TACCAACCTC TGTCCCTACA GGGCAGCCCC GAGAACCACA

1801  GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG AACCAGGTCA

1851  GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG

1901  TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT

1951  GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA

2001  AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG

2051  GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGGTAA

2101  ATGAGTGCGA CGGCCGGCAA GCCCCCGCTC CCCGGGCTCT CGCGGTCGCA

2151  CGAGGATGCT TGGCACGTAC CCCCTGTACA TACTTCCCGG GCGCCCAGCA

2201  TGGAAATAAA GCACCCAGCG CTGCCCTGGG CCCCTGCGAG ACTGTGATGG

2251  TTCTTTCCAC GGGTCAGGCC GAGTCTGAGG CCTGAGTGGC ATGAGGGAGG

2301  CAGAGCGGGT CCCACTGTCC CCACACTGGC CCAGGCTGTG CAGGTGTGCC

2351  TGGGCCCCCT AGGGTGGGGC TCAGCCAGGG GCTGCCCTCG GCAGGGTGGG

2401  GGATTTGCCA GCGTGGCCCT CCCTCCAGCA GCACCTGCCC TGGGCTGGGC

2451  CACGGGAAGC CCTAGGAGCC CCTGGGGACA GACACACAGC CCCTGCCTCT

2501  GTAGGAGACT GTCCTGTTCT GTGAGCGCCC CTGTCCTCCC GACCTCCATG

2551  CCCACTCGGG GGCATGCCTA GTCCATGTGC GTAGGGACAG GCCCTCCCTC

2601  ACCCATCTAC CCCCACGGCA CTAACCCCTG GCTGCCCTGC CCAGCCTCGC

2651  ACCCGCATGG GGACACAACC GACTCCGGGG ACATGCACTC TCGGGCCCTG

2701  TGGAGGGACT GGTGCAGATG CCCACACACA CACTCAGCCC AGACCCGTTC

2751  AACAAACCCC GCACTGAGGT TGGCCGGCCA CACGGCCACC ACACACACAC

2801  GTGCACGCCT CACACACGGA GCCTCACCCG GGCGAACTGC ACAGCACCCA
```

FIGURE 18B (SEQ ID NO. 22)

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2851  GACCAGAGCA  AGGTCCTCGC  ACACGTGAAC  ACTCCTCGGA  CACAGGCCCC

2901  CACGAGCCCC  ACGCGGCACC  TCAAGGCCCA  CGAGCCTCTC  GGCAGCTTCT

2951  CCACATGCTG  ACCTGCTCAG  ACAAACCCAG  CCCTCCTCTC  ACAAGGGTGC

3001  CCCTGCAGCC  GCCACACACA  CACAGGGGAT  CACACACCAC  GTCACGTCCC

3051  TGGCCCTGGC  CCACTTCCCA  GTGCCGCCCT  TCCCTGCAGG  ACGGATCAGC

3101  CTCGACTGTG  CCTTCTAGTT  GCCAGCCATC  TGTTGTTTGC  CCCTCCCCCG

3151  TGCCTTCCTT  GACCCTGGAA  GGTGCCACTC  CCACTGTCCT  TTCCTAATAA

3201  AATGAGGAAA  TTGCATCGCA  TTGTCTGAGT  AGGTGTCATT  CTATTCTGGG

3251  GGGTGGGGTG  GGGCAGGACA  GCAAGGGGGA  GGATTGGGAA  GACAATAGCA

3301  GGCATGCTGG  GGATGCGGTG  GGCTCTATGG  CTTCTGAGGC  GGAAAGAACC

3351  AGCTGGGGCT  CTAGGGGGTA  TCCCCACGCG  CCCTGTAGCG  GCGCATTAAG

3401  CGCGGCGGGT  GTGGTGGTTA  CGCGCAGCGT  GACCGCTACA  CTTGCCAGCG

3451  CCCTAGCGCC  CGCTCCTTTC  GCTTTCTTCC  CTTCCTTTCT  CGCCACGTTC

3501  GCCGGGCCTC  TCAAAAAAGG  GAAAAAAGC   ATGCATCTCA  ATTAGTCAGC

3551  AACCATAGTC  CCGCCCCTAA  CTCCGCCCAT  CCCGCCCCTA  ACTCCGCCCA

3601  GTTCCGCCCA  TTCTCCGCCC  CATGGCTGAC  TAATTTTTTT  TATTTATGCA

3651  GAGGCCGAGG  CCGCCTCGGC  CTCTGAGCTA  TTCCAGAAGT  AGTGAGGAGG

3701  CTTTTTTGGA  GGCCTAGGCT  TTTGCAAAAA  GCTTGGACAG  CTCAGGGCTG

3751  CGATTCGCG   CCAAACTTGA  CGGCAATCCT  AGCGTGAAGG  CTGGTAGGAT

3801  TTTATCCCCG  CTGCCATCAT  GGTTCGACCA  TTGAACTGCA  TCGTCGCCGT

3851  GTCCCAAAAT  ATGGGGATTG  GCAAGAACGG  AGACCTACCC  TGGCCTCCGC

3901  TCAGGAACGA  GTTCAAGTAC  TTCCAAAGAA  TGACCACAAC  CTCTTCAGTG

3951  GAAGGTAAAC  AGAATCTGGT  GATTATGGGT  AGGAAAACCT  GGTTCTCCAT

4001  TCCTGAGAAG  AATCGACCTT  TAAAGGACAG  AATTAATATA  GTTCTCAGTA

4051  GAGAACTCAA  AGAACCACCA  CGAGGAGCTC  ATTTTCTTGC  CAAAAGTTTG

4101  GATGATGCCT  TAAGACTTAT  TGAACAACCG  GAATTGGCAA  GTAAAGTAGA

4151  CATGGTTTGG  ATAGTCGGAG  GCAGTTCTGT  TTACCAGGAA  GCCATGAATC

4201  AACCAGGCCA  CCTTAGACTC  TTTGTGACAA  GGATCATGCA  GGAATTTGAA

4251  AGTGACACGT  TTTTCCCAGA  AATTGATTTG  GGGAAATATA  AACTTCTCCC

4301  AGAATACCCA  GGCGTCCTCT  CTGAGGTCCA  GGAGGAAAAA  GGCATCAAGT
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FIGURE 18C (SEQ ID NO. 22)

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4351  ATAAGTTTGA AGTCTACGAG AAGAAAGACT AACAGGAAGA TGCTTTCAAG

4401  TTCTCTGCTC CCCTCCTAAA GCTATGCATT TTTATAAGAC CATGGGACTT

4451  TTGCTGGCTT TAGATCTCTT TGTGAAGGAA CCTTACTTCT GTGGTGTGAC

4501  ATAATTGGAC AAACTACCTA CAGAGATTTA AAGCTCTAAG GTAAATATAA

4551  AATTTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT TGTTTGTGTA

4601  TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC

4651  CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG

4701  ATGAGGCTAC TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA

4751  AAGGTAGAAG ACCCCAAGGA CTTTCCTTCA GAATTGCTAA GTTTTTTGAG

4801  TCATGCTGTG TTTAGTAATA GAACTCTTGC TTGCTTTGCT ATTTACACCA

4851  CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA AAAATATTCT

4901  GTAACCTTTA TAAGTAGGCA TAACAGTTAT AATCATAACA TACTGTTTTT

4951  TCTTACTCCA CACAGGCATA GAGTGTCTGC TATTAATAAC TATGCTCAAA

5001  AATTGTGTAC CTTTAGCTTT TTAATTTGTA AAGGGGTTAA TAAGGAATAT

5051  TTGATGTATA GTGCCTTGAC TAGAGATCAT AATCAGCCAT ACCACATTTG

5101  TAGAGGTTTT ACTTGCTTTA AAAAACCTCC CACACCTCCC CCTGAACCTG

5151  AAACATAAAA TGAATGCAAT TGTTGTTGTT AACTTGTTTA TTGCAGCTTA

5201  TAATGGTTAC AAATAAAGCA ATAGCATCAC AAATTTCACA AATAAAGCAT

5251  TTTTTTCACT GCATTCTAGT TGTGGTTTGT CCAAACTCAT CAATGTATCT

5301  TATCATGTCT GGATCGGCTG GATGATCCTC CAGCGCGGGG ATCTCATGCT

5351  GGAGTTCTTC GCCCACCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA

5401  AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG

5451  CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG

5501  TATACCGTCG ACCTCTAGCT AGAGCTTGGC GTAATCATGG TCATAGCTGT

5551  TTCCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAA CATACGAGCC

5601  GGAAGCATAA AGTGTAAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC

5651  ATTAATTGCG TTGCGCTCAC TGCCCGCTTT CCAGTCGGGA AACCTGTCGT

5701  GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG CGGTTTGCGT

5751  ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT

5801  TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT
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FIGURE 18D (SEQ ID NO. 22)

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5851  CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG

5901  CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG

5951  GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT

6001  GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC

6051  TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC

6101  CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA

6151  GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC

6201  GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT

6251  TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG

6301  GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG

6351  AAGTGGTGGC CTAACTACGG CTACACTAGA AGGACAGTAT TTGGTATCTG

6401  CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT

6451  CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG

6501  CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC

6551  TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTTGG

6601  TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA

6651  TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG

6701  TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC

6751  GTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG

6801  GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG

6851  CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG

6901  AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT

6951  TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA

7001  CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA

7051  TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC

7101  CCCATGTTGT GCAAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT

7151  CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG GCAGCACTGC

7201  ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT

7251  GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG

7301  CTCTTGCCCG GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT
```

FIGURE 18E (SEQ ID NO. 22)

FIGURE 19 A
(SEQ ID NO. 23)

pD17-hG1b

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        10          20          30          40          50          60
GGTACCAATT  TAAATTGATA  TCTCCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA
CCATGGTTAA  ATTTAACTAT  AGAGGAATCC  AGAGCTCAGA GATCTATTGG CCAGTTAGCT

        70          80          90         100         110         120
TTGGAATTCT  TGCGGGCCGCT TGCTAGCACC AAGGGCCCAT CGGTCTTCCC CCTGGCACCC
AACCTTAAGA  ACGCCCGGCGA ACGATCGTGG TTCCCGGGTA GCCAGAAGGG GGACCGTGGG

       130         140         150         160         170         180
TCCTCCAAGA  GCACCTCTGG  GGGCACAGCG GCCCTGGGCT GCCTGGTCAA GGACTACTTC
AGGAGGTTCT  CGTGGAGACC  CCCGTGTCGC CGGGACCCGA CGGACCAGTT CCTGATGAAG

       190         200         210         220         230         240
CCCGAACCGG  TGACGGTGTC  GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC
GGGCTTGGCC  ACTGCCACAG  CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG

       250         260         270         280         290         300
CCGGCTGTCC  TACAGTCCTC  AGGACTCTAC TCCCTCAGCA GCGTGGTCAC CGTGCCCTCC
GGCCGACAGG  ATGTCAGGAG  TCCTGAGATG AGGGAGTCGT CGCACCAGTG GCACGGGAGG

       310         320         330         340         350         360
AGCAGCTTGG  GCACCCAGAC  CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG
TCGTCGAACC  CGTGGGTCTG  GATGTAGACG TTGCACTTAG TGTTCGGGTC GTTGTGGTTC

       370         380         390         400         410         420
GTGGACAAGA  AAGTTGGTGA  GAGGCCAGCA CAGGGAGGGA GGGTGTCTGC TGGAAGCCAG
CACCTGTTCT  TTCAACCACT  CTCCGGTCGT GTCCCTCCCT CCCACAGACG ACCTTCGGTC

       430         440         450         460         470         480
GCTCAGCGCT  CCTGCCTGGA  CGCATCCCGG CTATGCAGCC CCAGTCCAGG GCAGCAAGGC
CGAGTCGCGA  GGACGGACCT  GCGTAGGGCC GATACGTCGG GGTCAGGTCC CGTCGTTCCG

       490         500         510         520         530         540
AGGCCCCGTC  TGCCTCTTCA  CCCGGGAGGCC TCTGCCCGCC CCACTCATGC TCAGGGGAGAG
TCCGGGGCAG  ACGGAGAAGT  GGGCCTCCGG AGACGGGCGG GGTGAGTACG AGTCCCCTCTC

       550         560         570         580         590         600
GGTCTTCTGG  CTTTTTTCCCC AGGCTCTGGG CAGGCACAGG CTAGGTGCCC CTAACCCAGG
CCAGAAGACC  GAAAAAAGGGG TCCGAGACCC GTCCGTGTCC GATCCACGGG GATTGGGTCC
```

FIGURE 19B
(SEQ ID NO. 23)

pD17-hG1b

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610                 620                 630                 640                 650                 660
CCCTGCACAC  AAAGGGGGCAG  GTGCTGGGCT  CAGACCTGCC  AAGAGCCATA  TCCGGGGAGGA
GGGACGTGTG  TTTCCCCGTC  CACGACCCGA  GTCTGGACGG  TTCTCGGTAT  AGGCCCTCCT

670                 680                 690                 700                 710                 720
CCCTGCCCCT  GACCTAAGCC  CACCCCAAAG  GCCAAAACTCT  CCACTCCCTC  AGCTCGGACA
GGGACGGGGA  CTGGATTCGG  GTGGGGTTTC  CGGTTTGAGA  GGTGAGGGAG  TCGAGCCTGT

730                 740                 750                 760                 770                 780
CCTTCTCTCC  TCCCAGATTC  CAGTAACTCC  CAATCTTCTC  TCTGCAGAGC  CCAAATCTTG
GGAAGAGAGG  AGGGTCTAAG  GTCATTGAGG  GTTAGAAGAG  AGACGTCTCG  GGTTTAGAAC

790                 800                 810                 820                 830                 840
TGACAAAACT  CACACATGCC  AGGTAAGCCA  GCCCAGGGCCT  CGCCCTCCAG
ACTGTTTTGA  GTGTGTACGG  GTGGCACGGG  TCCATTCGGT  CGGGTCCGGA  GCGGGAGGTC

850                 860                 870                 880                 890                 900
CTCAAGGCGG  GACAGGTGCC  CTAGAGTAGC  CTGCATCCAG  GGACAGGCCC  CAGCCCGGGTG
GAGTTCCGCC  CTGTCCACGG  GATCTCATCG  GACGTAGGTC  CCTGTCCGGG  GTCGGGCCCAC

910                 920                 930                 940       235         950  237        960
CTGACACGTC  CACCTCCATC  TCTTCCTCAG  CACCTGAACT  GCTGGGGGGA  CCGTCAGTCT
GACTGTGCAG  GTGGAGGTAG  AGAAGGAGTC  GTGGACTTGA  CGACCCCCCT  GGCAGTCAGA

970                 980                 990                 1000                1010                1020
TCCTCTTCCC  CCCAAAACCC  AAGGACACCC  TCATGATCTC  CCGGACCCCT  GAGGTCACAT
AGGAGAAGGG  GGGTTTTGGG  TTCCTGTGGG  AGTACTAGAG  GGCCTGGGGA  CTCCAGTGTA

1030                1040                1050                1060                1070                1080
GCGTGGTGGT  GGACGTGAGC  CACGAAGACC  CTGAGGTCAA  GTTCAACTGG  TACGTGGACG
CGCACCACCA  CCTGCACTCG  GTGCTTCTGG  GACTCCAGTT  CAAGTTGACC  ATGCACCTGC

1090                1100                1110                1120                1130                1140
GCGTGGAGGT  GCATAATGCC  AAGACAAAGC  CGCGGGAGGA  GCAGTACAAC  AGCACGTACC
CGCACCTCCA  CGTATTACGG  TTCTGTTTCG  GCGCCCTCCT  CGTCATGTTG  TCGTGCATGG

1150                1160                1170        318                1180                1190   318              320    1200
GTGCTGGTCAG  CGTCCTCACC  GTCCTGCAGG  AGGACTGGCT  GAATGGCAAG  GAGTACAAGT
CACACCAGTC  GCAGGAGTGG  CAGGACGTGG  TCCTGACCGA  CTTACCGTTC  CTCATGTTCA
```

FIGURE 19C
(SEQ ID NO. 23)

pD17-hG1b

```
1210        1220        1230
GCAGGTCTC   CAACAAAGCC  CTCCCAGCGC
CGTTCCAGAG  GTTGTTTCGG  GAGGGTCGGG

1240        1250        1260
CCATCGAGAA  AACCATCTCC  AAAGCCAAAG
GGTAGCTCTT  TTGGTAGAGG  TTTCGGTTTC

1270        1280        1290        1300        1310        1320
GTGGGACCCG  TGGGGTGCGA  GGGCCACATG  GACAGAGGCC  GGCTCGGCCC  ACCCTCTGCC
CACCCTGGGC  ACCCCACGCT  CCCGGTGTAC  CTGTCTCCGG  CCGAGCCGGG  TGGGAGACGG

1330        1340        1350        1360        1370        1380
CTGAGAGTGA  CCGGCTGTACC AACCTCTGTC  CCTACAGGGC  AGCCCGGAGA  ACCACAGGTG
GACTCTCACT  GGCGACATGG  TTGGAGACAG  GGATGTCCCG  TCGGGGCTCT  TGGTGTCCAC

1390        1400        1410        1420        1430        1440
TACACCCTGC  CCCCATCCCG  GGATGAGCTG  ACCAAGAACC  AGGTCAGCCT  GACCTGCCTG
ATGTGGGACG  GGGGTAGGGC  CCTACTCGAC  TGGTTCTTGG  TCCAGTCGGA  CTGGACGGAC

1450        1460        1470        1480        1490        1500
GTCAAAGGCT  TCTATCCCAG  CGACATCGCC  GTGGAGTGGG  AGAGCAATGG  GCAGCCGGAG
CAGTTTCCGA  AGATAGGGTC  GCTGTAGCGG  CACCTCACCC  TCTCGTTACC  CGTCGGCCTC

1510        1520        1530        1540        1550        1560
AACAACTACA  AGACCACGCC  TCCCGTGCTG  GACTCCGACG  GCTCCTTCTT  CCTCTACAGC
TTGTTGATGT  TCTGGTGCGG  AGGGCACGAC  CTGAGGCTGC  CGAGGAAGAA  GGAGATGTCG

1570        1580        1590        1600        1610        1620
AAGCTCACCG  TGGACAAGAG  CAGGTGGCAG  CAGGGGAACG  TCTTCTCATG  CTCCGTGATG
TTCGAGTGGC  ACCTGTTCTC  GTCCACCGTC  GTCCCCTTGC  AGAAGAGTAC  GAGGCACTAC

1630        1640        1650        1660        1670        1680
CATGAGGCTC  TGCACAACCA  CTACACGCAG  AAGAGCCTCT  CCCTGTCTCC  GGGTAAATGA
GTACTCCGAG  ACGTGTTGGT  GATGTGCGTC  TTCTCGGAGA  GGGACAGAGG  CCCATTTACT

1690        1700        1710        1720        1730        1740
GTGGCGACGGC CGGCGAAGCCC CCGGCTCCCG GGCTCTGCGG GTCGCACGAG GATGCTTGGC
CACGCTGCCG  GCCGTTCGGG  GGCGAGGGGC CCGAGAGCGC CAGCGTGCTC CTACGAACCG

1750        1760        1770        1780        1790        1800
GTGGACGGGC  TGTACACTACT TCCCGGGGCGC CCAGCATGGA  GATGCTTGGC  CCAGCGCCTGC
CACGCTGCCG  ACATGTATGA  AGGGCCCGCG  TTATTTCGTG  GGTCGCGGACG

1750        1760        1770        1780        1790        1800
ACGTACCCCC  TGTACACTACT TCCCGGGGCGC CCAGCATGGA  CCAGCGCCTGC
TGCATGGGGG  ACATGTATGA  AGGGCCCGCG  TTATTTCGTG  GGTCGCGGACG
```

FIGURE 19D
(SEQ ID NO. 23)

pD17-hG1b

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        1810       1820       1830       1840       1850       1860
  CCTGGGCCCC TGCGAGACTG TGATGGTTCT TTCCACGGGT CAGGCCGAGT CTGAGGCCTG
  GGACCCGGGG ACGCTCTGAC ACTACCAAGA AAGGTGCCCA GTCCGGCTCA GACTCCGGAC

        1870       1880       1890       1900       1910       1920
  AGTGGCATGA GGGAGGCAGA GCGGGTCCCA CTGTCCCCAC ACTGGCCCAG GCTGTGCAGG
  TCACCGTACT CCCTCCGTCT CGCCCAGGGT GACAGGGGTG TGACCGGGTC CGACACGTCC

        1930       1940       1950       1960       1970       1980
  TGTGCCCTGG GCCCCCTAGG GTGGGGCTCA GCCAGGGGCT GCCCTCGGCA GGGTGGGGGA
  ACACGGGACC CGGGGGATCC CACCCCGAGT CGGTCCCCGA CGGGAGCCGT CCCACCCCCT

        1990       2000       2010       2020       2030       2040
  TTGCCAGCGT GGCCCTCCCT CCAGCAGCAC CTGCCCCTGG CTGGGCCACG GGAAGCCCTA
  AACGGTCGCA CCGGGAGGGA GGTCGTCGTG GACGGGGACC GACCCGGTGC CCTTCGGGAT

        2050       2060       2070       2080       2090       2100
  GGAGCCCCTG GGGACAGACA CACAGCCCCT GCCTCTGTAG GAGACTGTCC TGTTCTGTGA
  CCTCGGGGAC CCCTGTCTGT GTGTCGGGGA CGGAGACATC CTCTGACAGG ACAAGACACT

        2110       2120       2130       2140       2150       2160
  GCGCCCCTGT CCTCCCGACC TCCATGCCCA CTCGGGGGCA TGCTGGGGAT GCGGTGGGCT
  CGCGGGGACA GGAGGGCTGG AGGTACGGGT GAGCCCCCGT ACGACCCCTA CGCCACCCGA

        2170       2180       2190       2200       2210       2220
  CTATGGCTTC TGAGGCGGAA AGAACCAGCT GGGGGCTCTAG GGGGTATCCC CACGCGCCCT
  GATACCGAAG ACTCCGCCTT TCTTGGTCGA CCCCGAGATC CCCATAGGG GTGCGCGGGA

        2230       2240       2250       2260       2270       2280
  GTAGCGGCGC ATTAAGCGCG GGCGGTGTGG TGGTTACGCG CAGGGTGACC GCTACACTTG
  CATCGCCGCG TAATTCGCGC CCGCCACACC ACCAATGCGC GTCCCACTGG CGATGTGAAC

        2290       2300       2310       2320       2330       2340
  CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC CAGCGTGACC ACGTTCGCCG
  GGTCGCGGGA TCGCGGGCGA GGAAAGCGAA AGAAGGGAAG GTCGCACTGG TGCAAGCGGC

        2350       2360       2370       2380       2390       2400
  GCTTTCCCCG TCAAGCTCTA AATCGGGGCA TCCCTTTAGG GTTCCGATTT AGTGCTTTAC
  CGAAAGGGGC AGTTCGAGAT TTAGCCCCGT AGGGAAATCC CAAGGCTAAA TCACGAAATG
```

FIGURE 19E
(SEQ ID NO. 23)

pD17-hG1b

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      2410        2420        2430        2440        2450        2460
      GGCACCTCGA  CCCAAAAAAA  CTTGATTAGG  GTGATGGTTC  ACGTAGTGGG  CCATCGCCCT
      CCGTGGAGCT  GGGGTTTTTT  GAACTAATCC  CACTACCAAG  TGCATCACCC  GGTAGCGGGA

      2470        2480        2490        2500        2510        2520
      GATAGACGGT  TTTTCGCCCT  TTGACGTTGG  AGTCCACGTT  CTTTAATAGT  GGACTCTTGT
      CTATCTGCCA  AAAAGCGGGA  AACTGCAACC  TCAGGTGCAA  GAAATTATCA  CCTGAGAACA

      2530        2540        2550        2560        2570        2580
      TCCAAACTGG  AACAACACTC  CGGTCTATTC  TTTTGATTTA  TAAGGGATTT
      AGGTTTGACC  TTGTTGTGAG  GCCAGATAAG  AAAACTAAAT  ATTCCCTAAA

      2590        2600        2610        2620        2630        2640
      TGGGGATTTC  GGCCTATTGG  TTAAAAAATG  AGCTGATTTA  ACAAAAATTT  AACGCGAATT
      ACCCCTAAAG  CCGGATAACC  AATTTTTTAC  TCGACTAAAT  TGTTTTTAAA  TTGCGCTTAA

      2650        2660        2670        2680        2690        2700
      AATTCTGTGG  AATGTGTGTC  AGTTAGGGTG  TGGAAAGTCC  CCAGGCTCCC  CAGGCAGGCA
      TTAAGACACC  TTACACACAG  TCAATCCCAC  ACCTTTCAGG  GGTCCGAGGG  GTCCGTCCGT

      2710        2720        2730        2740        2750        2760
      GAAGTATGCA  AAGCATGCAT  CTCAATTAGT  CAGCAACCAT  AGTCCCGCCC  CTAACTCCGC
      CTTCATACGT  TTCGTACGTA  GAGTTAATCA  GTCGTTGGTA  TCAGGGCGGG  GATTGAGGCG

      2770        2780        2790        2800        2810        2820
      CCATCCCGCC  CCTAACTCCG  CCCAGTTCCG  CCCATTCTCC  GCCCCATGGC  TGACTAATTT
      GGTAGGGCGG  GGATTGAGGC  GGGTCAAGGC  GGGTAAGAGG  CGGGGTACCG  ACTGATTAAA

      2830        2840        2850        2860        2870        2880
      TTTTTATTTA  TGCAGAGGCC  GAGGCCGCCT  CGGCCTCTGA  GCTATTCCAG  AAGTAGTGAG
      AAAAATAAAT  ACGTCTCCGG  CTCCGGCGGA  GCCGGAGACT  CGATAAGGTC  TTCATCACTC

      2890        2900        2910        2920        2930        2940
      GAGGCTTTTT  TGGAGGGCTA  GGCTTTTGCA  AAAAGCTTGG  ACAGCTCAGG  GCTGCGATTT
      CTCCGAAAAA  ACCTCCCGAT  CCGAAAACGT  TTTTCGAACC  TGTCGAGTCC  CGACGCTAAA

      2950        2960        2970        2980        2990        3000
      CGGCGCCAAAC TTGACGGGCAA TCCTAGCGTG  GGATTTTTATC CCCGCTGCCA
      GCGCGGTTTG  AACTGCCCGTT AGGATCGCAC  CCTAAAAATAG GGGCGACGGT
```

FIGURE 19F
(SEQ ID NO. 23)

pD17-hG1b

```
3010        3020        3030        3040        3050        3060
TCATGGTTCG  ACCATTGAAC  TGCATCGTCG  CCGTGTCCCA  AAATATGGGG  ATTGGCAAGA
AGTACCAAGC  TGGTAACTTG  ACGTAGCAGC  GGCACAGGGT  TTTATACCCC  TAACCGTTCT

3070        3080        3090        3100        3110        3120
ACGGAGACCT  ACCCTGGCCT  CCGCTCAGGA  ACGAGTTCAA  GTACTTCCAA  AGAATGACCA
TGCCTCTGGA  TGGGACCGGA  GGCGAGTCCT  TGCTCAAGTT  CATGAAGGTT  TCTTACTGGT

3130        3140        3150        3160        3170        3180
CAACCTCTTC  AGTGGAAGGT  AAACAGAATC  TGGTGATTAT  GGGTAGGAAA  ACCTGGTTCT
GTTGGAGAAG  TCACCTTCCA  TTTGTCTTAG  ACCACTAATA  CCCATCCTTT  TGGACCAAGA

3190        3200        3210        3220        3230        3240
CCATTCCTGA  GAAGAATCGA  CCTTTAAAGG  ACAGAATTAA  TATAGTTCTC  AGTAGAGAAC
GGTAAGGACT  CTTCTTAGCT  GGAAATTTCC  TGTCTTAATT  ATATCAAGAG  TCATCTCTTG

3250        3260        3270        3280        3290        3300
TCAAAGAACC  ACCACGAGGA  GCTCATTTTC  TTGCCAAAAG  TTTGGATGAT  GCCTTAAGAC
AGTTCTTTGG  TGGTGCTCCT  CGAGTAAAAG  AACGGTTTTC  AAACCTACTA  CGGAATTCTG

3310        3320        3330        3340        3350        3360
TTATTGAACA  ACCGGAATTG  GCAAGTAAAG  TAGACATGGT  TTGGATAGTC  GGGAGGCAGTT
AATAACTTGT  TGGCCTTAAC  CGTTCATTTC  ATCTGTACCA  AACCTATCAG  CCCTCCGTCAA

3370        3380        3390        3400        3410        3420
CTGTTTACCA  GGAAGCCATG  AATCAACCAG  GCCACCTTAG  ACTCTTTGTG  ACAAGGATCA
GACAAATGGT  CCTTCCGGTAC  TTAGTTGGTC  CGGTGGAATC  TGAGAAACAC  TGTTCCTAGT

3430        3440        3450        3460        3470        3480
TGCAGGAATT  TGAAAGTGAC  ACGTTTTTCC  CAGAAATTGA  TTTGGGGAAA  TATAAACTTC
ACGTCCTTAA  ACTTTCACTG  TGCAAAAAGG  GTCTTTAACT  AAACCCCTTT  ATATTTGAAG

3490        3500        3510        3520        3530        3540
TCCCAGAATA  CCCAGGCGTC  CTCTCTGAGG  TCCAGGAGGA  AAAAGGCATC  AAGTATAAGT
AGGGTCTTAT  GGGTCCGCAG  GAGAGACTCC  AGGTCCTCCT  TTTTCCGTAG  TTCATATTCA

3550        3560        3570        3580        3590        3600
TTGAAGTCTA  CGAGAAGAAA  GACTAACAGG  AAGATGCTTT  CAAGTTCTCT  GCTCCCCTCC
AACTTCAGAT  GCTCTTCTTT  CTGATTGTCC  TTCTACGAAA  GTTCAAGAGA  CGAGGGGAGG
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FIGURE 19G
(SEQ ID NO. 23)

pD17-hG1b

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3610       3620       3630       3640       3650       3660
TAAAGCTATC CATTTTTATA AGACCATGGG ACTTTTGCTG GCTTTAGATC TCTTTGTGAA
ATTTCGATAC GTAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT

3670       3680       3690       3700       3710       3720
GGAACCTTAC TTCTGTGGTG TGACATAATT GGACAAACTA CCTACAGAGA TTTAAAGCTC
CCTTGGAATG AAGACACCAC ACTGTATTAA CCTGTTTGAT GGATGTCTCT AAATTTCGAG

3730       3740       3750       3760       3770       3780
TAAGGTAAAT ATAAAAATTT TAAGTGTATA ATGTGTTAAA CTACTGAATC TAATTGTTTG
ATTCCATTTA TATTTTTAAA ATTCACATAT TACACAATTT GATGACTTAG ATTAACAAAC

3790       3800       3810       3820       3830       3840
TGTTATTTTAG ATTCCAACCT ATGGAACTGA TGAATGGGAG CAGTGGTGGA ATGCCTTTAA
ACATAAAATC TAAGGTTGGA TACCTTGACT ACTTACCCTC GTCACCACCT TACGGAAATT

3850       3860       3870       3880       3890       3900
TGAGGAAAAC CTGTTTTGCT CAGAAGAAAT GCCATCTAGT GATGATGAGG CTACTGCTGA
ACTCCTTTTG GACAAAACGA GTCTTCTTTA CGGTAGATCA CTACTACTCC GATGACGACT

3910       3920       3930       3940       3950       3960
CTCTCAACAT TCTTACTCCTC CAAAAAAGAA GAGAAAAGGTA GAAGACCCCA AGGACTTTCC
GAGAGTTGTA AGATGAGGAG GTTTTTTCTT CTCTTTTCCAT TCTTCTGGGGT TCCTGAAAGG

3970       3980       3990       4000       4010       4020
TTCAGAATTG CTAAGTTTTT TGAGTCATGC TGTGTTTTAGT AATAGAAACTC TTGCCTTGCTT
AAGTCTTAAC GATTCAAAAA ACTCAGTACG ACACAAATCA TTATCTTGAG AACGACGAA

4030       4040       4050       4060       4070       4080
TGCTATTTAC ACCACAAAGG AAAAAAGCTGC ACTGCTATAC AAGAAAAATTA TGGAAAAATA
ACGATAAATG TGGTGTTTCC TTTTTTCGACG TGACGATATG TTCTTTTTAAT ACCTTTTTAT

4090       4100       4110       4120       4130       4140
TTCTGTAACC TTTTATAAGTA GGCATAACAG TTATAAATCAT AACATACTGT TTTTTTCTTAC
AAGACATTGG AAATATTCAT CCGTATTGTC AATATTAGTA TTGTATGACA AAAAAGAATG

4150       4160       4170       4180       4190       4200
TCCACACAGG CATAGAGTGT CTGCTATTAA TAACTATGCT CAAAAAATTGT GTACCCTTTAG
AGGTGTGTCC GTATCTCACA GACGATAATT ATTGATACGA GTTTTTTAACA CATGGAAATC
```

FIGURE 19H
(SEQ ID NO. 23)

pD17-hG1b

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4210        4220       4230       4240       4250       4260
CTTTTTAATT  TGTAAAGGGG TTAATAAGGA ATATTTGATG TATAGTGCCT TGACTAGAGA
GAAAAATTAA  ACATTCCCC  AATTATTCCT TATAAACTAC ATATCACGGA ACTGATCTCT

4270        4280       4290       4300       4310       4320
TCATAATCAG  CCATACCACA TTTGTAGAGG TTTTACTTGC TTTTAAAAAC CTCCCACACC
AGTATTAGTC  GGTATGGTGT AAACATCTCC AAAATGAACG AAAATTTTTG GAGGGTGTGG

4330        4340       4350       4360       4370       4380
TCCCCCTGAA  CCTGAAACAT AAAATGAATG TCACAAATTT TGTTAACTTG TTTATTGCAG
AGGGGGACTT  GGACTTGTA  TTTTACTTAC ACAATTGAAC AAATAACGTC

4390        4400       4410       4420       4430       4440
CTTATAAATGG TTACAAATAA AGCAAATAGCA TCACAAATAAA GCATTTTTTT
GAATATTACC AATGTTTATT TCGTTATCGT AGTGTTTAAA GTGTTTATTT CGTAAAAAAA

4450        4460       4470       4480       4490       4500
CACTGCAATTC TAGTTGTGGT TTGTCCAAAC TCATCAAATGT ATCTTATCAT GTCTGGATCG
GTGACGTAAG ATCAACACA  AACAGGTTTG AGTAGTTACA TAGAATAGTA CAGACCTAGC

4510        4520       4530       4540       4550       4560
GCTCGGATGAT CCTCCAGCGC GGGGATCTCA TGCTGGAGTT CTTCGCCCAC CCCAACTTGT
CGACCTACTA GGAGGTCGCG CCCCTAGAGT ACGACCTCAA GAAGCGGGTG GGGTTGAACA

4570        4580       4590       4600       4610       4620
TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAAATTTC ACAAATAAAG
AATAACGTCG AATATTACCA ATGTTTATTT CGTTATCGTA GTGTTTAAAG TGTTTATTTC

4630        4640       4650       4660       4670       4680
CATTTTTTTC ACTGCAATTCT AGTTGTGGTT TGTCCAAACT CATCAAATGTA TCTTATCATG
GTAAAAAAG TGACGTTAGA TCAACACCAA ACAGGTTTGA GTAGTTTACAT AGAATAGTAC

4690        4700       4710       4720       4730       4740
TCTGTATACC GTCGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCTG
AGACATATGG CAGCTGGAGA TCGATCTCGA ACCGCATTAG TACCAGTATC GACAAAGGAC

4750        4760       4770       4780       4790       4800
TGTGAAATTG TTATCCGGCTC ACAATTCCAC ACAACATACG AGCCGGAAGC ATAAAGTGTA
ACACTTTAAC AATAGGCGAG TGTTGTCATG TCGGCCTTCG TATTTCACAT
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FIGURE 19I
(SEQ ID NO. 23)

pD17-hG1b

```
         4810       4820       4830       4840       4850       4860
    AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG
    TTCGGACCCC ACGGATTACT CACTCGATTG AGTGTAATTA ACGCAACGCG AGTGACGGGC

         4870       4880       4890       4900       4910       4920
    CTTTCCAGTC GGGAAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGCGCGGGGA
    GAAAGGTCAG CCCTTTGGAC AGCACGGTCG ACGTAATTAC TTAGCCGGTT GCGCGCCCCT

         4930       4940       4950       4960       4970       4980
    GAGGCGGTTT GCGTATTGGG CGCTCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG
    CTCCGCCAAA CGCATAACCC GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC

         4990       5000       5010       5020       5030       5040
    TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
    AGCAAGCCGA CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC

         5050       5060       5070       5080       5090       5100
    AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC
    TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC CGGTCCTTGG

         5110       5120       5130       5140       5150       5160
    GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCCTGAC GAGCATCACA
    CATTTTTCCG GCGCAAACGAC CGCAAAAAGG TATCCGAGGC GGGGGGACTG CTCGTAGTGT

         5170       5180       5190       5200       5210       5220
    AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT
    TTTTAGCTGC GAGTTCAGTC TCCACCGCTT TGGGCTGTCC TGATATTTCT ATGGTCCGCA

         5230       5240       5250       5260       5270       5280
    TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC
    AAGGGGGACC TTCGAGGGAG CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG

         5290       5300       5310       5320       5330       5340
    TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA ATGCTCACGC TGTAGGTATC
    ACAGGCGGAA AGAGGGAAGC CCTTCGCACC CGCGAAAGAGT TACGAGTGCG ACATCCATAG

         5350       5360       5370       5380       5390       5400
    TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAG
    AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG GGGCAAGTCG
```

FIGURE 19J
(SEQ ID NO. 23)

pD17-hG1b

```
5410        5420        5430        5440        5450        5460
CCGACCGCTG  CGCCTTATCC  GGTAACTATC  GTCTTGAGTC  CAACCCGGTA  AGACACGACT
GGCTGGCGAC  GCGGAATAGG  CCATTGATAG  CAGAACTCAG  GTTGGGCCAT  TCTGTGCTGA

5470        5480        5490        5500        5510        5520
TATCCGCCACT GGCAGCAGCC ACTGGTAACA GGAATTAGCAG AGCGAGGTAT GTAGGCGGGTG
ATAGCGGGTGA CCGTCGTCGG TGACCAATGT CCTAATCGTC TCGCTCCATA CATCCGCCAC

5530        5540        5550        5560        5570        5580
CTACAGAGTT  CTTGAAGTGG  TGGCCTAACT  ACGGCTACAC  TAGAAGGACA  GTATTTGGTA
GATGTCTCAA  GAACTTCACC  ACCGGATTGA  TGCCGATGTG  ATCTTCCTGT  CATAAACCAT

5590        5600        5610        5620        5630        5640
TCTGCGCTCT  GCTGAAGCCA  GTTACCTTCG  GAAAAAGAGT  TGGTAGCTCT  TGATCCGGCA
AGACGCGAGA  CGACTTCGGT  CAATGGAAGC  CTTTTTCTCA  ACCATCGAGA  ACTAGGCCGT

5650        5660        5670        5680        5690        5700
AACAAACCAC  CGCTGGTAGC  GGTGGTTTTT  TTGTTTGCAA  GCAGCAGATT  ACGCGCAGAA
TTGTTTGGTG  GCGACCATCG  CCACCAAAAA  AACAAACGTT  CGTCGTCTAA  TGCGCGTCTT

5710        5720        5730        5740        5750        5760
AAAAAGGATC  TCAAGAAGAT  CCTTTGATCT  TTTCTACGGG  GTCTGACGCT  CAGTGGAACG
TTTTTCCTAG  AGTTCTTCTA  GGAAACTAGA  AAAGATGCCC  CAGACTGCGA  GTCACCTTGC

5770        5780        5790        5800        5810        5820
AAAACTCACG  TTAAGGGATT  TTGGTCATGA  GATTATCAAA  AAGGATCTTC  ACCTAGATCC
TTTTGAGTGC  AATTCCCTAA  AACCAGTACT  CTAATAGTTT  TTCCTAGAAG  TGGATCTAGG

5830        5840        5850        5860        5870        5880
TTTTAAATTA  AAAATGAAGT  TTTAAATCAA  TCTAAAGTAT  ATATGAGTAA  ACTTGGTCTG
AAAATTTAAT  TTTTACTTCA  AAATTTAGTT  AGATTTCATA  TATACTCATT  TGAACCAGAC

5890        5900        5910        5920        5930        5940
ACAGTTACCA  ATGCTTAATC  AGTGAGGCAC  CTATCTCAGC  GATCTGTCTA  TTTCGTTCAT
TGTCAATGGT  TACGAATTAG  TCACTCCGTG  GATAGAGTCG  CTAGACAGAT  AAAGCAAGTA

5950        5960        5970        5980        5990        6000
CCATAGTTGC  CTGACTCCCC  GTCGTGTAGA  TAACTACGAT  ACGGGAGGGC  TTACCATCTG
GGTATCAACG  GACTGAGGGG  CAGCACATCT  ATTGATGCTA  TGCCCTCCCG  AATGGTAGAC
```

FIGURE 19K
(SEQ ID NO. 23)

pD17-hG1b

```
        6010       6020       6030       6040       6050       6060
   GCCCCAGTGC TGCAATGATA CCGCGAGACC CACGGCTCACC GGCTCCAGAT TTATCAGCAA
   CGGGGTCACG ACGTTACTTAT GGCGCTCTGG GTGCCGAGTGG CCGAGGTCTA AATAGTCGTT

        6070       6080       6090       6100       6110       6120
   TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA
   ATTTGGTCGG TCGGCCTTCC CGGCTCGCGT CTTCACCAGG ACGTTGAAAT AGGCGGAGGT

        6130       6140       6150       6160       6170       6180
   TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC
   AGGTCAGATA ATTAACAACG GCCCTTCGAT CTCATTCATC AAGCGGTCAA TTATCAAACG

        6190       6200       6210       6220       6230       6240
   GCAACGTTGT TGCCATTGCT ACAGGCATCG TGGTGTCACG CTCGTCGTTT GGTATGGCTT
   CGTTGCAACA ACGGTAACGA TGTCCGTAGC ACCACAGTGC GAGCAGCAAA CCATACCGAA

        6250       6260       6270       6280       6290       6300
   CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA
   GTAAGTCGAG GCCAAGGGTT GCTAGTTCCG CTCAATGTAC TAGGGGGTAC AACACGTTTT

        6310       6320       6330       6340       6350       6360
   AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTTAT
   TTCGCCAATC GAGGAAGCCA GGAGGCTAGC AACAGTCTTC ATTCAACCGG CGTCACAATA

        6370       6380       6390       6400       6410       6420
   CACTCATGGT TATGGCAGCA CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT
   GTGAGTACCA ATACCGTCGT GACGTATTAA GAGAATGACA GTACGGTAGG CATTCTACGA

        6430       6440       6450       6460       6470       6480
   TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA
   AAAGACACTG ACCACTCATG AGTTGGTTCA GTAAGACTCT TATCACATAC GCCGCTGGCT

        6490       6500       6510       6520       6530       6540
   GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG
   CAACGAGAAC GGGCCGCAGT TATGCCCTAT TATGGCGCGG TGTATCGTCT TGAAATTTTC

        6550       6560       6570       6580       6590       6600
   TGCTCATCAT TGGAAAACGT TCTTCGGGGC GAAAACTCTC AAGGATCTTA CCGCTGTTGA
   ACGAGTAGTA ACCTTTTGCA AGAAGCCCCG CTTTTGAGAG TTCCTAGAAT GGCGACAACT
```

FIGURE 19L
(SEQ ID NO. 23)

pD17-hG1b

```
     6610       6620       6630       6640       6650       6660
GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCCATCT TTTACTTTCA
CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG AAGTCGGTAGA AAATGAAAGT

     6670       6680       6690       6700       6710       6720
CCAGCCGTTTC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG
GGTCGGCAAAG ACCCACTCGT TTTTGTCCTT CCGTTTTACG GCGTTTTTTC CCTTATTCCC

     6730       6740       6750       6760       6770       6780
CGACACGGAA ATGTTGAATA CTCATACTCT TCCTTTTTCA ATATTATTGA AGCATTTATC
GCTGTGCCTT TACAACTTAT GAGTATGAGA AGGAAAAAGT TATAATAACT TCGTAAATAG

     6790       6800       6810       6820       6830       6840
AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC

     6850       6860       6870       6880       6890       6900
GGGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT CGAGGGGATCG GGAGATCTGC
CCCAAGGCGC GTGTAAAGGG GCTTTTTCACG GTGGACTGCA GCTCCCTAGC CCTCTAGACG

     6910       6920       6930       6940       6950       6960
TAGGTTGACCT GAGGCGCGCC GGCTTCGAAT AGCCCAGAGTA ACCTTTTTTT TTAATTTTAT
ATCCACTGGA CTCCGCGCGG CCGAAGCTTA TCGGGTCTCAT TGGAAAAAAA AATTAAAATA

     6970       6980       6990       7000       7010       7020
TTTATTTTAT TTTTGAGATG GAGTTTGGCG CCGATCTCCC GATCCCCTAT GGTCGACTCT
AAATAAAATA AAAACTCTAC CTCAAACCGC GGCTAGAGGG CTAGGGGATA CCAGCTGAGA

     7030       7040       7050       7060       7070       7080
CAGTACAATC TGCTCTCGAT CCGCAATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT
GTCATGTTAG ACGAGACTAC GGCGTTATCA TTCGGTCATA GACGAGGGAC GAACACACAA

     7090       7100       7110       7120       7130       7140
GGGAGGTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTTGACCGA
CCTCCAGCGA CTCATCACGC GCTCGTTTTA AATTCGATGT TGTTCCGTTC CGAACTGGCT

     7150       7160       7170       7180       7190       7200
CAATTGCATG AAGAAATCTGC TTAGGGTTAG GCGTTTTGCG CTGCTTCGCG ATGTACGGGC
GTTAACGTAC TTCTTAGACG AATCCCAATC CGCAAAACGC GACGAAGCGC TACATGCCCG
```

FIGURE 19M
(SEQ ID NO. 23)

pD17-hG1b

```
7210       7220       7230       7240       7250       7260
CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC
GTCTATATGC GCAACTGTAA CTAATAACTG ATCAATAATT AATGCCCCAG

7270       7280       7290       7300       7310       7320
ATTAGTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC
TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT GAATGCCATT TACCGGGCGG

7330       7340       7350       7360       7370       7380
TGGCTGACCG CCCAACGACC CCCGCCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
ACCGACTGGC GGGTTGCTGG GGGCGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA

7390       7400       7410       7420       7430       7440
AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAC TATTTACGGT AAACTGCCCA
TTGCGGTTAT CCCTGAAAGG TAACTGCAGT TACCCACCTG ATAAATGCCA TTTGACGGGT

7450       7460       7470       7480       7490       7500
CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC CCTATTGACG TCAATGACGG
GAACCGTCAT GTAGTTCACA TAGTATACGG TTCATGCGGG GGATAACTGC AGTTACTGCC

7510       7520       7530       7540       7550       7560
TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA
ATTTACCGGG CGGACCGTAA TACGGGTCAT GTACTGGAAT ACCCTGAAAG GATGAACCGT

7570       7580       7590       7600       7610       7620
GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA
CATGTAGATG CATAATCAGT AGCGATAATG GTACCACTAC GCCAAAACCG TCATGTAGTT

7630       7640       7650       7660       7670       7680
TGGGCGTGGA TAGCCGGTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
ACCCGCACCT ATCGGCCAAC TGAGTGCCCC TAAAGGTTCA GAGGTGGGGT AACTGCAGTT

7690       7700       7710       7720       7730       7740
TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC
ACCCTCAAAC AAAACCGTGG TTTTAGTTGC CCTGAAAGGT TTTACAGCAT TGTTGAGGCG

7750       7760       7770       7780       7790       7800
CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT
GGGTAACTGC GTTTACCCGC CATCCGCACA TGCCACCCTC CAGATATATT CGTCTCGAGA
```

FIGURE 19N
(SEQ ID NO. 23)

pD17-hG1b

```
    7810       7820       7830       7840       7850       7860
CTGGCTAACT AGAGAACCCA CTGGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG
GACCGATTGA TCTCTTGGGT GACGAATGAC CGAATAGCTT TAATTATGCT GAGTGATATC

    7870       7880
GGAGACCCAA GCTT
CCTCTGGGTT CGAA
```

Figure 26

hBR96-2 Heavy Chain Variable Region (V$_H$)

```
1          11          21          31          41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY
51          61          71          81          91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL
101         111
ADGAWFAYWG QGTLVTVSS   (SEQ ID NO. 24)
```

human IgG1 constant

```
                        |CH1
                        A STKGPSVFPL APSSKSTSGG TAALGCLVKD

YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY

                                    |CH2 235 237
ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPEILGGP SVFLFPPKPK

DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
                    318 320 322       334      |CH3
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV

YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL

DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
```

                                    (SEQ ID NO. 25)

Figure 27

hBR96-2A: Heavy Chain Variable Region (V_H)

```
1           11          21          31          41
EVQLVESGGG  LVQPGGSLRL  SCAASGFPFS  DYYMYWVRQA  PGKGLEWVSY

51          61          71          81          91
ISQDGDITDY  ADSVKGRFTI  SRDNAKNSLY  LQMNSLRDED  TAVYYCARGL

101         111
ADGAWFAYWG  QGTLVTVSS  (SEQ ID NO. 24)
```

hBR96-2A: Human Heavy Chain IgG1 Constant Region ΔCH2

```
A STKGPSVFPL  APSSKSTSGG  TAALGCLVKD  YFPEPVTVSW  NSGALTSGVH

  TFPAVLQSSG  LYSLSSVVTV  PSSSLGTQTY  ICNVNHKPSN  TKVDKKVEPK

  SCDKTHTCPP  CP    GQPREPQV  YTLPPSRDEL  TKNQVSLTCL  VKGFYPSDIA

  VEWESNGQPE  NNYKTTPPVL  DSDGSFFLYS  KLTVDKSRWQ  QGNVFSCSVM

  HEALHNHYTQ  KSLSLSPGK  (SEQ ID NO. 26)
```

Figure 28

This sequence is the chi BR96 IgG1 with CH2 deleted.

VH
```
  1   EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYYMYWVRQT PEKRLEWVAY
 51   ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARGL
101   DDGAWFAYWG QGTLVTVSVA STKGPSVFPL APSSKSTSGG TAALGCLVKD
151   YPPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
201   ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPGQPREPQV YTLPPSRDEL
251   TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS
301   KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
```
CH1 (above position 101 region, near STKGPSVFPL)

CH3 (above position 201 region, near GQPREPQV)

(SEQ ID NO. 27)